

[illegible]

ctc	tac	ctg	gtc	ttc	ggc	gca	gtg	gtc	ttc	tcc	tcg	gtg	gag	ctg	ccc	323
Leu	Tyr	Leu	Val	Phe	Gly	Ala	Val	Val	Phe	Ser	Ser	Val	Glu	Leu	Pro	
			35					40					45			

tat	gag	gac	ctg	ctg	cgc	cag	gag	ctg	cgc	aag	ctg	aag	cga	cgc	ttc	371
Tyr	Glu	Asp	Leu	Leu	Arg	Gln	Glu	Leu	Arg	Lys	Leu	Lys	Arg	Arg	Phe	
		50					55					60				
ttg	gag	gag	cac	gag	tgc	ctg	tct	gag	cag	cag	ctg	gag	cag	ttc	ctg	419
Leu	Glu	Glu	His	Glu	Cys	Leu	Ser	Glu	Gln	Gln	Leu	Glu	Gln	Phe	Leu	
	65					70					75					
ggc	cgg	gtg	ctg	gag	gcc	agc	aac	tac	ggc	gtg	tcg	gtg	ctc	agc	aac	467
Gly	Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	
	80				85				90						95	
gcc	tcg	ggc	aac	tgg	aac	tgg	gac	ttc	acc	tcc	gcg	ctc	ttc	ttc	gcc	515
Ala	Ser	Gly	Asn	Trp	Asn	Trp	Asp	Phe	Thr	Ser	Ala	Leu	Phe	Phe	Ala	
			100						105					110		
agc	acc	gtg	ctc	tcc	acc	aca	ggc	tat	ggc	cac	acc	gtg	ccc	ttg	tca	563
Ser	Thr	Val	Leu	Ser	Thr	Thr	Gly	Tyr	Gly	His	Thr	Val	Pro	Leu	Ser	
			115					120					125			
gat	gga	ggc	aag	gcc	ttc	tgc	atc	atc	tac	tcc	gtc	att	ggc	att	ccc	611
Asp	Gly	Gly	Lys	Ala	Phe	Cys	Ile	Ile	Tyr	Ser	Val	Ile	Gly	Ile	Pro	
			130				135					140				
ttc	acc	ctc	ctg	ttc	ctg	acg	gct	gtg	gtc	cag	cgc	atc	acc	gtg	cac	659
Phe	Thr	Leu	Leu	Phe	Leu	Thr	Ala	Val	Val	Gln	Arg	Ile	Thr	Val	His	
			145				150				155					
gtc	acc	cgc	agg	ccg	gtc	ctc	tac	ttc	cac	atc	cgc	tgg	ggc	ttc	tcc	707
Val	Thr	Arg	Arg	Pro	Val	Leu	Tyr	Phe	His	Ile	Arg	Trp	Gly	Phe	Ser	
					165					170					175	
aag	cag	gtg	gtg	gcc	atc	gtc	cat	gcc	gtg	ctc	ctt	ggg	ttt	gtc	act	755
Lys	Gln	Val	Val	Ala	Ile	Val	His	Ala	Val	Leu	Leu	Gly	Phe	Val	Thr	
				180					185					190		
gtg	tcc	tgc	ttc	ttc	ttc	atc	ccg	gcc	gct	gtc	ttc	tca	gtc	ctg	gag	803
Val	Ser	Cys	Phe	Phe	Phe	Ile	Pro	Ala	Ala	Val	Phe	Ser	Val	Leu	Glu	
			195					200					205			
gat	gac	tgg	aac	ttc	ctg	gaa	tcc	ttt	tat	ttt	tgt	ttt	att	tcc	ctg	851
Asp	Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	
		210					215					220				
agc	acc	att	ggc	ctg	ggg	gat	tat	gtg	cct	ggg	gaa	ggc	tac	aat	caa	899
Ser	Thr	Ile	Gly	Leu	Gly	Asp	Tyr	Val	Pro	Gly	Glu	Gly	Tyr	Asn	Gln	
			225			230					235					
aaa	ttc	aga	gag	ctc	tat	aag	att	ggg	atc	acg	tgt	tac	ctg	cta	ctt	947
Lys	Phe	Arg	Glu	Leu	Tyr	Lys	Ile	Gly	Ile	Thr	Cys	Tyr	Leu	Leu	Leu	
					245					250					255	
ggc	ctt	att	gcc	atg	ttg	gta	gtt	ctg	gaa	acc	ttc	tgt	gaa	ctc	cat	995
Gly	Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	
				260					265					270		
gag	ctg	aaa	aaa	ttc	aga	aaa	atg	ttc	tat	gtg	aag	aag	gac	aag	gac	1043
Glu	Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	
			275					280					285			
gag	gat	cag	gtg	cac	atc	ata	gag	cat	gac	caa	ctg	tcc	ttc	tcc	tcg	1091

Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	Ala	
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Ser	Gly	Asn	Trp	Asn	Trp	Asp	Phe	Thr	Ser	Ala	Leu	Phe	Phe	Ala	Ser	
		100						105					110			
Thr	Val	Leu	Ser	Thr	Thr	Gly	Tyr	Gly	His	Thr	Val	Pro	Leu	Ser	Asp	
		115					120					125				
Gly	Gly	Lys	Ala	Phe	Cys	Ile	Ile	Tyr	Ser	Val	Ile	Gly	Ile	Pro	Phe	
	130					135					140					
Thr	Leu	Leu	Phe	Leu	Thr	Ala	Val	Val	Gln	Arg	Ile	Thr	Val	His	Val	
145					150					155					160	
Thr	Arg	Arg	Pro	Val	Leu	Tyr	Phe	His	Ile	Arg	Trp	Gly	Phe	Ser	Lys	
			165						170					175		
Gln	Val	Val	Ala	Ile	Val	His	Ala	Val	Leu	Leu	Gly	Phe	Val	Thr	Val	
			180					185					190			
Ser	Cys	Phe	Phe	Phe	Ile	Pro	Ala	Ala	Val	Phe	Ser	Val	Leu	Glu	Asp	
		195					200					205				
Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	Ser	
	210					215					220					
Thr	Ile	Gly	Leu	Gly	Asp	Tyr	Val	Pro	Gly	Glu	Gly	Tyr	Asn	Gln	Lys	
225					230					235					240	
Phe	Arg	Glu	Leu	Tyr	Lys	Ile	Gly	Ile	Thr	Cys	Tyr	Leu	Leu	Leu	Gly	
			245						250					255		
Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	Glu	
			260					265					270			
Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	Glu	
		275					280					285				
Asp	Gln	Val	His	Ile	Ile	Glu	His	Asp	Gln	Leu	Ser	Phe	Ser	Ser	Ile	
	290					295					300					
Thr	Asp	Gln	Ala	Ala	Gly	Met	Lys	Glu	Asp	Gln	Lys	Gln	Asn	Glu	Pro	
305					310					315					320	
Phe	Val	Ala	Thr	Gln	Ser	Ser	Ala	Cys	Val	Asp	Gly	Pro	Ala	Asn	His	
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<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (126)..(1307)

<220>
 <223> TASK

THE UNIVERSITY OF CHICAGO

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ggacg	atg	aag	cgg	cag	aac	gtg
Met	Lys	Arg	Gln	Asn	Val	Arg
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						15
ttc	acc	tac	ctg	ctg	gtg	ggc
Phe	Thr	Tyr	Leu	Leu	Val	Gly
			20			25
						30
gag	ccc	gag	ctg	atc	gag	cgg
Glu	Pro	Glu	Leu	Ile	Glu	Arg
			35			40
						45
ctg	cgg	gcg	cgc	tac	aac	ctc
Leu	Arg	Ala	Arg	Tyr	Asn	Leu
		50				55
						60
cgc	gtc	gtg	ctg	cgc	ctc	aag
Arg	Val	Val	Leu	Arg	Leu	Lys
	65					70
						75
ttc	gcc	ggc	tcc	ttc	tac	ttc
Phe	Ala	Gly	Ser	Phe	Tyr	Phe
80					85	
						90
tac	ggg	cac	gcg	gca	ccc	agc
Tyr	Gly	His	Ala	Ala	Pro	Ser
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						105
ttc	tac	gcg	ctg	ctg	ggc	atc
Phe	Tyr	Ala	Leu	Leu	Gly	Ile
			115			120
						125
ctg	ggc	gag	cgc	atc	aac	acc
Leu	Gly	Glu	Arg	Ile	Asn	Thr
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						140
aag	aag	ggg	ctg	ggc	atg	cgg
Lys	Lys	Gly	Leu	Gly	Met	Arg
	145					150
						155
gtg	ctc	atc	ggc	ttc	ttc	tcg
Val	Leu	Ile	Gly	Phe	Phe	Ser
160						165
						170
gcc	gcc	ttc	tcc	cac	tac	gag
Ala	Ala	Phe	Ser	His	Tyr	Glu
				180		
						185
tac	tgc	ttc	atc	acc	ctc	acc
Tyr	Cys	Phe	Ile	Thr	Leu	Thr
			195			200
						205
ctg	cag	aag	gac	cag	gcc	ctg
Leu	Gln	Lys	Asp	Gln	Ala	Leu
		210				215
						220

agc ttc gtc tac atc ctt acg ggc ctc acg gtc atc ggc gcc ttc ctc	842
Ser Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu	
225 230 235	
aac ctc gtg gtg ctg cgc ttc atg acc atg aac gcc gag gac gag aag	890
Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys	
240 245 250 255	
cgc gac gcc gag cac cgc gcg ctg ctc acg cgc aac ggg cag gcg ggc	938
Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly	
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ggc ggc gga ggg ggt ggc agc gcg cac act acg gac acc gcc tca tcc	986
Gly Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser	
275 280 285	
acg gcg gca gcg ggc ggc ggc ggc ttc cgc aac gtc tac gcg gag gtg	1034
Thr Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val	
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ctg cac ttc cag tcc atg tgc tgc tgc ctg tgg tac aag agc cgc gag	1082
Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu	
305 310 315	
aag ctg cag tac tcc atc ccc atg atc atc ccg cgg gac ctc tcc acg	1130
Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr	
320 325 330 335	
tcc gac acg tgc gtg gag cag agc cac tgc tgc ccg gga ggg ggc ggc	1178
Ser Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly	
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cgc tac agc gac acg ccc tgc cga cgc tgc ctg tgc agc ggg gcg cca	1226
Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro	
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cgc tcc gcc atc agc tgc gtg tcc acg ggt ctg cac agc ctg tcc acc	1274
Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr	
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Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val	
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caacctccct tcgtgttgtt ttgcatggct ttgcagttat ggagaaagtg gaaaccagc 1867	

agtccctaaa gctgggtcccc agaaagcagg acagaaagaa ggagggacag gcaggcagca 1927
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 aattaaccag gtgtgggtggc acgtgcctgg gagtcccagc gacttgggag gctgaggtgg 2407
 gaggattggt tgagcctggg aggtcgaggg tgtagtgagc cctgattgca ccactgtact 2467
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<210> 4

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<223> TASK

<400> 4

Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe
 1 5 10 15

Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
 20 25 30

Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu
 35 40 45

Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
 50 55 60

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
 65 70 75 80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95

Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
 100 105 110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
 115 120 125

Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
 130 135 140

Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val

145		150		155		160
Leu Ile Gly Phe	Phe Ser Cys Ile Ser	Thr Leu Cys Ile Gly	Ala Ala			
	165	170	175			
Ala Phe Ser His	Tyr Glu His Trp Thr	Phe Phe Gln Ala	Tyr Tyr Tyr			
	180	185	190			
Cys Phe Ile Thr	Leu Thr Thr Ile Gly	Phe Gly Asp Tyr	Val Ala Leu			
	195	200	205			
Gln Lys Asp Gln	Ala Leu Gln Thr Gln	Pro Gln Tyr Val	Ala Phe Ser			
	210	215	220			
Phe Val Tyr Ile	Leu Thr Gly Leu Thr	Val Ile Gly Ala	Phe Leu Asn			
	225	230	235			240
Leu Val Val Leu	Arg Phe Met Thr Met	Asn Ala Glu Asp	Glu Lys Arg			
	245	250	255			
Asp Ala Glu His	Arg Ala Leu Leu Thr	Arg Asn Gly Gln	Ala Gly Gly			
	260	265	270			
Gly Gly Gly Gly	Gly Ser Ala His Thr Thr	Asp Thr Ala Ser	Ser Thr			
	275	280	285			
Ala Ala Ala Gly	Gly Gly Gly Phe Arg	Asn Val Tyr Ala	Glu Val Leu			
	290	295	300			
His Phe Gln Ser	Met Cys Ser Cys Leu	Trp Tyr Lys Ser	Arg Glu Lys			
	305	310	315			320
Leu Gln Tyr Ser	Ile Pro Met Ile Ile	Pro Arg Asp Leu	Ser Thr Ser			
	325	330	335			
Asp Thr Cys Val	Glu Gln Ser His Ser	Ser Pro Gly Gly	Gly Gly Arg			
	340	345	350			
Tyr Ser Asp Thr	Pro Ser Arg Arg	Cys Leu Cys Ser	Gly Ala Pro	Arg		
	355	360	365			
Ser Ala Ile Ser	Ser Val Ser Thr	Gly Leu His Ser	Leu Ser Thr	Phe		
	370	375	380			
Arg Gly Leu Met	Lys Arg Arg Ser	Ser Val				
	385	390				

<210> 5
 <211> 405
 <212> PRT
 <213> Murine

<220>
 <223> TASK

<400> 5
 Glu Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu
 1 5 10 15
 Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met

20 25 30
 Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg
 35 40 45
 Tyr Asn Leu Ser Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu
 50 55 60
 Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser
 65 70 75 80
 Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala
 85 90 95
 Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu
 100 105 110
 Leu Gly Ile Pro Leu Thr Leu Ile Met Phe Gln Ser Leu Gly Glu Arg
 115 120 125
 Ile Asn Thr Phe Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu
 130 135 140
 Gly Met Arg His Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly
 145 150 155 160
 Phe Val Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser
 165 170 175
 Tyr Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile
 180 185 190
 Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp
 195 200 205
 Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser Phe Val Tyr
 210 215 220
 Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn Leu Val Val
 225 230 235 240
 Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu
 245 250 255
 His Arg Ala Leu Leu Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly
 260 265 270
 Leu Ser Cys Leu Ser Gly Ser Leu Gly Asp Val Arg Pro Arg Asp Pro
 275 280 285
 Val Thr Cys Ala Ala Ala Ala Gly Gly Val Gly Val Gly Val Gly Gly
 290 295 300
 Ser Gly Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met
 305 310 315 320
 Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile
 325 330 335
 Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu
 340 345 350

His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro
 355 360 365
 Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser
 370 375 380
 Val Ser Thr Gly Leu His Ser Leu Ala Ala Phe Arg Gly Leu Met Lys
 385 390 395 400
 Arg Arg Ser Ser Val
 405

<210> 6
 <211> 347
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: TWIK-1 homolog

<400> 6

Met Tyr Thr Asp Glu Gly Glu Tyr Ser Gly Asp Thr Asp His Gly Gly
 1 5 10 15
 Ser Thr Met Gln Lys Met Ser Pro Asn Thr Arg Gln Asn Phe Arg Gln
 20 25 30
 Asn Val Asn Val Val Val Cys Leu Ser Ala Ala Ile Thr Leu Leu Val
 35 40 45
 Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn
 50 55 60
 Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His
 65 70 75 80
 Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu
 85 90 95
 Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala
 100 105 110
 Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu
 115 120 125
 Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu
 130 135 140
 Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe
 145 150 155 160
 Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val
 165 170 175
 Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr
 180 185 190
 Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu
 195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser
 210 215 220
 Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr
 225 230 235 240
 Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp
 245 250 255
 Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn
 260 265 270
 Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile
 275 280 285
 Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln
 290 295 300
 Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln
 305 310 315 320
 Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn
 325 330 335
 Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr
 340 345

<210> 7

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: TWIK-1 homolog

<400> 7

Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala
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 Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys
 20 25 30
 Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys
 35 40 45
 Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His
 50 55 60
 Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp
 65 70 75 80
 Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser
 85 90 95
 Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu
 100 105 110
 Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu
 115 120 125

Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg
 20 25 30
 Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser
 35 40 45
 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val
 50 55 60
 Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile
 65 70 75 80
 Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser
 85 90 95
 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
 100 105 110
 Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
 115 120 125
 Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
 130 135 140
 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
 145 150 155 160
 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Glu Gly Phe Leu Leu Ala Gly
 165 170 175
 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
 180 185 190
 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
 195 200 205
 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
 210 215 220
 Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
 225 230 235 240
 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
 245 250 255
 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
 260 265 270
 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
 275 280 285
 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
 290 295 300
 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
 305 310 315 320
 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
 325 330 335

<210> 12
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> TOK-1 P1

<400> 12
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly
1 5 10 15
Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
20 25

<210> 13
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
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Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
20 25

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<220>
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representative K+ channel sequence

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1 5 10 15
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representative K⁺ channel sequence

<220>
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1 5 10 15
Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly
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representative K⁺ channel sequence

<220>
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<400> 16
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Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly
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<210> 17
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representative K⁺ channel sequence

<220>
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<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
1 5 10 15
Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly
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<210> 18

<211> 27
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<220>
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representative K+ channel sequence

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<400> 18
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1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu
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<210> 19
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representative K+ channel sequence

<220>
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<400> 19
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu
20 25

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<220>
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representative K+ channel sequence

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<400> 20
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly
1 5 10 15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu
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<210> 21
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representative K⁺ channel sequence

<220>
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<400> 21
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly
1 5 10 15
Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala
20 25

<210> 22
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<212> PRT
<213> Unknown

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Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro
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<210> 23
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1 5 10 15
Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro
20 25

<210> 24
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